

10/677,977

=====  
Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Wed Sep 05 15:35:32 EDT 2007  
=====

\*\*\*\*\*

Reviewer Comments:

<210> 6

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<220>

<221> Variant

<222> (1)..(1)

<223> Wherein Xaa is an N-acetyl group.

<220>

<221> Variant

<222> (6)..(6)

<223> Wherein Xaa is a 7-amino-4-methylcoumarin group.

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Xaa Ile Glu Pro Asp Xaa

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5

The above explanations for Xaa are invalid: "Xaa" can only represent a  
single amino acid, not a functional group.

<210> 29

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<212> PRT

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The above <223> explanation for "Xaa" at location 4 contains a misspelling: please replace "or" with "or."

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Validated By CRFValidator v 1.0.3

Application No: 10677977

Version No: 4.0

Input Set:

Output Set:

Started: 2007-08-23 14:48:11.063

Finished: 2007-08-23 14:48:11.915

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 852 ms

Total Warnings: 3

Total Errors: 3

No. of SeqIDs Defined: 57

Actual SeqID Count: 57

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
E 257	Invalid sequence data feature in <221> in SEQ ID (22)
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E 341	'Xaa' position not defined SEQID (54) POS (2)

# SEQUENCE LISTING

<110> Nguyen, Jack  
 Thanos, Chris  
 Waugh Ruggles, Sandra  
 Craik, Charles S.

<120> METHODS OF GENERATING AND SCREENING FOR PROTEASES WITH ALTERED  
 SPECIFICITY

<130> 19049-005001/4905

<140> 10677977

<141> 2003-10-02

<150> 60/425,388

<151> 2002-10-02

<160> 57

<170> FastSEQ for Windows Version 4.0

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Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser  
 20 25 30

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 35 40 45

Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg  
 50 55 60

Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn  
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Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile  
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Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser  
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Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile  
145 150 155 160

Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser  
165 170 175

Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Asp Ala Asp  
180 185 190

Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn  
195 200 205

Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys  
210 215 220

Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn  
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Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe  
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The above "<222> 3" is an incorrect location for "Xaa:" "Leu" is at location 3; "Xaa" is at location 2.

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Xaa Xaa Xaa Xaa

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Xaa Xaa Leu Xaa

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